

SEQUENCE LISTENING



<110> Dahlqvist, Anders
Stahl, Ulf
Lenman, Marit
Banas, Antoni
Ronne, Hans
Stymne, Sten

<120> PROCESSES FOR PRODUCING TRIACYLGLYCEROL USING GENES THAT ENCODE PHOSPHOLIPID:DIACYLGLYCEROL ACYLTRANSFERASES

<130> BASFnae337799PCT1-15

<140> US 09/937779

<150> PCT / EP 00 / 02701

<151> 2000-03-23

<160> 32

<170> PatentIn Ver. 3.3

<210> 1

<211> 1986

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1983)

<400> 1

atg	ggc	aca	ctg	ttt	cga	aga	aat	gtc	cag	aac	caa	aag	agt	gat	tct	48
Met	Gly	Thr	Leu	Phe	Arg	Arg	Asn	Val	Gln	Asn	Gln	Lys	Ser	Asp	Ser	
1															15	

gat	gaa	aac	aat	aaa	ggg	ggt	tct	gtt	cat	aac	aag	cga	gag	agc	aga	96
Asp	Glu	Asn	Asn	Lys	Gly	Gly	Ser	Val	His	Asn	Lys	Arg	Glu	Ser	Arg	
20															30	

aac	cac	att	cat	cat	caa	cag	gga	tta	ggc	cat	aag	aga	aga	agg	ggt	144
Asn	His	Ile	His	His	Gln	Gln	Gly	Leu	Gly	His	Lys	Arg	Arg	Arg	Gly	
35															45	

att	agt	ggc	agt	gca	aaa	aga	aat	gag	cgt	ggc	aaa	gat	ttc	gac	agg	192
Ile	Ser	Gly	Ser	Ala	Lys	Arg	Asn	Glu	Arg	Gly	Lys	Asp	Phe	Asp	Arg	
50															60	

aaa	aga	gac	ggg	aac	ggt	aga	aaa	cgt	tgg	aga	gat	tcc	aga	aga	ctg	240
Lys	Arg	Asp	Gly	Asn	Gly	Arg	Lys	Arg	Trp	Arg	Asp	Ser	Arg	Arg	Leu	
65															80	

att	ttc	att	ctt	ggg	gca	ttc	tta	ggt	gta	ctt	ttg	ccg	ttt	agc	ttt	288
Ile	Phe	Ile	Leu	Gly	Ala	Phe	Leu	Gly	Val	Leu	Leu	Pro	Phe	Ser	Phe	
85															95	

ggc	gct	tat	cat	gtt	cat	aat	agc	gat	agc	gac	ttg	ttt	gac	aac	ttt	336
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe			
100	105	110	
gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt			384
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val			
115	120	125	
ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac			432
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn			
130	135	140	
tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt			480
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly			
145	150	155	160
aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta			528
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val			
165	170	175	
atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att			576
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile			
180	185	190	
gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg			624
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp			
195	200	205	
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg			672
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp			
210	215	220	
ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac			720
Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn			
225	230	235	240
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc			768
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile			
245	250	255	
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att			816
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile			
260	265	270	
ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt			864
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu			
275	280	285	
gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag			912
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys			
290	295	300	
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta			960
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu			
305	310	315	320
att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg			1008
Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp			

	325	330	335	
gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val	340	345	350	1056
aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly	355	360	365	1104
gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr	370	375	380	1152
att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser	385	390	395	1200
400				
aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser	405	410	415	1248
420				
atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser	425	430	435	1296
440				
tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att Ser Glu Asp Ala Leu Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile	435	440	445	1344
450				
cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met	455	460	465	1392
470				
aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctccaa Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln	465	475	480	1440
485				
aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu	490	495	500	1488
505				
gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met	500	505	510	1536
515				
gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr	515	520	525	1584
530				
ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp	530	535	540	1632
545				
gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro	545	550	555	1680
560				

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser 565 570 575	1728
atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly 580 585 590	1776
att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp 595 600 605	1824
ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser 610 615 620	1872
gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp 625 630 635 640	1920
ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln 645 650 655	1968
atg ccc ttc cca atg taa Met Pro Phe Pro Met 660	1986
<210> 2	
<211> 661	
<212> PRT	
<213> <i>Saccharomyces cerevisiae</i>	
<400> 2	
Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser 1 5 10 15	
Asp Glu Asn Asn Lys Gly Ser Val His Asn Lys Arg Glu Ser Arg 20 25 30	
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly 35 40 45	
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg 50 55 60	
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu 65 70 75 80	
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe 85 90 95	
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe 100 105 110	

Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430

Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445

Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480

Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495

Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525

Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540

Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560

Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605

Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

Met Pro Phe Pro Met
 660

<210> 3

<211> 2312

<212> genomic DNA

<213> Schizosaccharomyces pombe

<400> 3

atggcgtctt ccaagaagag caaaaactcat aagaaaaaga aagaagtcaa atctcctatc 60
 gacttaccaa attcaaagaa accaactcgc gctttgagtg agcaaccc 120

tttcaaataa	atcaagaaaa	tctaaatttg	aaaaaaagatt	gaattttata	180
ttttgggat	atgcggtgct	tttttttcg	ctgttggaga	cgacaatgt	240
gttttcgacc	ctgctacgtt	ggaaatatgc	taggccttc	agacttgtt	300
gatgacatta	aaggataattt	gtgtttaagg	atgcacccctt	tactacggac	360
aaggccttcgc	agtctcctag	gttcaagttt	gtcttgatat	gtacaatgag	420
ggatatcgaa	gtgaccatcc	tgtttattatg	ttatcagctc	aggatttagaa	480
agttggtcgt	ttaataattt	tacttttagga	aacgtctttt	ggtagctgg	540
tctatgctga	aggcaatgtt	cattgacaag	caatgtggc	ttgaacattt	600
aaaaaaaaaccg	gcttggatcc	gaagggattt	aagctgcgag	cagctcaggg	660
gctgttatttt	ttatcacggg	ctattggatt	tggagtaaaag	taattgaaaaa	720
atgggttatg	agcctaataa	catgttaagt	gottcttacg	atggcgggtt	780
aatttagagg	aacgtgataa	atattttca	aagttaaaaaa	tgttcattga	840
attgtacata	agaaaaaaggt	agtgttgatt	tctcactcca	tgggttcaca	900
tatttttta	agtggttga	agctgagggc	tacggaaatg	gtggaccgac	960
gatcatattt	aagcatttt	aatgtgagt	ctcgatgggt	gtttgactac	1020
tttgaataga	tatcgggatc	tttgatttga	gcacccaaaa	cagtggcagc	1080
ggtgaaatga	aagatacagg	tattgttaatt	acattaaaca	tgttaatatt	1140
taaccgtttt	aagctcaattt	gaatcagttt	tccgtctatg	ggtaagcaat	1200
gatttggttac	taatttactg	tttagtttgg	aaaaattttt	ttcccgttct	1260
caaaaataca	aatgtgctct	actttttcta	acttttaata	gagagccatg	1320
ctatgggagg	agttagttct	atgcttccct	aaggaggcga	tgttgtatgg	1380
gttgggttaag	aaatatgtgc	tgttaatttt	ttattaatat	ttaggctcca	1440
atcaaacaaa	tttttccaat	ggtgcaatta	ttcgatataag	agaagacatt	1500
acgatgaatt	tgacatagat	gatgcattac	aatttttaaa	aatgttaca	1560
ttaaaagtcat	gctagcgaaa	aattttccc	acggtcttgc	ttggactgaa	1620
taaaaaataaa	cgaaaatgccg	tctaaatgg	taaatccgt	agaagtaaga	1680
tactaaattt	tactaaccca	aatagactag	tcttccttat	gctcctgata	1740
ttgcgttcac	gggggtcgaa	aaccaactga	gagaggttat	tattatacta	1800
ggggcaacct	gtcattgatt	cctcggttaa	tgttggaaaca	aaagtgtaaa	1860
atttatgttt	caaacattct	attaactgtt	ttatttaggtt	attgttatgg	1920
tggaaacttta	ccaatatttag	cccttggttt	ggtgtgcaat	aaagtttggc	1980
gtttaatcct	gctaatacaca	gtatcacaaa	ttatgaaatc	aagcatgaac	2040
tgtatctgaga	ggaggacctc	gctcgccaga	acacgtcgat	ctgctgcgtt	2100
aaatgtatgt	tcatTTTacc	ttacaaattt	cttactacta	atacttggac	2160
ttttaaaagt	ttcatcaggc	catggtgact	cggttacaaa	attcagagct	2220
agtacggaca	taagtttgt	agattgcaat	taactaacta	accgaacagg	2280
atgagataaa	tctcgataaa	ccttagaaatt	aa		2312

```
<210> 4
<211> 3685
<212> genomic DNA
<213> Arabidopsis thaliana
```

```
<400> 4
atgcccctta ttcatcgaa aaagccgacg gagaaaccat cgacgccgc atctgaagag 60
gtggtcacg atgaggattc gcaaaaagaaa ccacacgaaat cttccaaatc ccaccataag 120
aaatcgaaacg gaggagggaa gtggtcgtgc atcgattctt gttgttggtt cattgggtgt 180
gtgtgttaa cctgggtgtt tcttctctt ctttacaacg caatgcctgc gagcttcct 240
cagtagttaa cgagcgaat cacgggtctt ttgcctgacc cggccgggtgt taagctaaaa 300
aaagaaggtc ttaaggcgaa acatcctgtt gtcttcattc ctgggattgt caccgggtggg 360
ctcgagcttt gggaaaggcaa acaatgcgcgt gatggtttat tttagaaaacg tttgtgggt 420
ggaacttttg gtgaagtcta caaaaaggta gctcaacaat tctcactctt cctttatatt 480
gggatttggaa ttggatctga tgagatcacg cacttgttgc ttcttcaaca tcactcaaac 540
tttaattcca tggatgtctg tcttactctt tactttttt tttttttgtat gtggaaacgc 600
attttcttaa gagactattt ctgtatgtgt aaggtaaggcg ttccaaggac gtaatttgct 660
tggactattt ctgtttgatt gttaacttta ggatataaaa tagctgcctt ggaatttcaa 720
```

gtcatcttat tgccaaatct gttgctagac atgccctaga gtccgttcat aacaagttac 780
ttccttact gtcgttgcgt gtagattag ctttgttag cgataatga agtagtgtt 840
tatgtttgt tggaaataga gaagttctaa ctacatctgt ggaaagtgt ttcaggctgt 900
gatagaggac tggcttta ttattcaact atgtatatgt gtaattaaag ctagttcc 960
tttgcattt cagctcaatg tgctttctc aattttttc tcaatttcaa agtttccat 1020
cgagttatt cacatgtctt gaatttgcgc catcctcggt ctgttatcca gcttgaact 1080
cctccgacc ctgctatgga tatattaaaa aaaaagtgtt ttgtgggtt catcttgc 1140
acgatctgca tcttcttctt tcggctcagt gtcatgttt ttgctatggt agagatggc 1200
aatgttattt tgatggtaa cagtggtata gtgtatagta tcttaactaa tcaattatct 1260
cttgattca ggcctctatg ttgggtggaa cacatgtcac ttgacaatga aactgggtt 1320
gatccagctg gtatttagagt tcgagctgtc tcaggactcg tggctgctga ctacttgc 1380
cctggctact ttgtctggc agtgctgatt gctaaccctt cacatattgg atatgaagag 1440
aaaaatatgt acatggctgc atatgactgg cggcttcgt ttcagaacac agaggttctt 1500
ttctcatcgt tcttcttattt attctgtcc atgttacgtt tcttcttca ttacttaagg 1560
cttaaatatg tttcatgtt aattaatagg tacgtgatca gactcttagc cgtatgaaaa 1620
gtaatataga ttgtatggtt tctaccaaacg gtggaaaaaa agcaggatata gttccgcatt 1680
ccatgggggt ctgttattttt ctacatttt tgaagtgggt tgaggcacca gtcctctgg 1740
gtggcggggg tggccagat ttgtgtgcaaa agtataattaa ggcggtgatg aacattgggt 1800
gaccatttct ttgtgttcca aaagctgtt cagggcttt ctctgtgaa gcaaggatg 1860
ttgcagttgc caggtattga atatctgtt atactttga tgatcagaac cttggctctg 1920
gaactcaaag ttattctact aaatatcaat tctaataaca ttgctatattt atcgtgc 1980
ctgacattgg ttgattattt ttgctgctt tgaactgaa actcttgc gattagacaa 2040
atgatgaatt gataattctt acgcattgtc ctgtgtatgac cagttctta gttcgac 2100
taacatttg catactgtct ttggaggcattt attgaattttt gctatggaaa ggcgtggagc 2160
ttccatgtctt gcatttctt ccaatttagcg ttattctgtc tcttcaattt ttcttgc 2220
tgcattctatg gtcttttattt tcttcttaat taaaagactcg ttggattagt tgctctattt 2280
gtcactttgtt cccttaatattt agaactttac ttcttcgaa aattgcagag cgattgcccc 2340
aggattctt gacaccgata tatttagact tcagacctt cagcatgtaa tgagaatgac 2400
acgcacatgg gactcaacaa tgtctatgtt accgaaggaa ggtgacacga tatggggcgg 2460
gtttgattgg tcacccggaga aaggccacac ctgttggggg aaaaagcaaa agaacaacga 2520
aacttgggtt gaagcagggtt aaaacggagt ttccaagaaa agtccgtt actatggaa 2580
gatgatatct ttggaaatgg aagttagcaga ggctgcgcctt tctgagatataatattga 2640
ttttcgagta aggacatata aatcataata aaccttgcattt attttgtatgatgatgatg 2700
atatctgtac attttatctt gtgaagggtt ctgtcaaaagg tcagagtatc ccaatcaca 2760
cctgtcgta cgtgtggaca gagtaccatg acatggaaat tgctggatc aaagctatcg 2820
ctgagttataa ggtctacact gctgggtgaag ctatagatctt actacattat gttgtcctta 2880
agatgtatggc gcgtggtgcc gtcattttctt ctatggaaat tgctgtatgatgatgac 2940
ccaagtatca agatccaaa tactggtcaa atccgttaga gacaaggtaa gtgatttctt 3000
gattccaaact gtatcctcg tcctgtatgc ttatcgttctt ttttgggtt ggtctgtt 3060
gatatggttt tcagctcaaa gcttacaaag ctgtttctgtc gccttctca aaaaggctt 3120
ctcagtaata ttgaggtgtt aaagttgata catgtgactc ttgcttataa atcctccgtt 3180
tggttgttc tgcttttca gattaccgaa tgctcctgatg atggaaatctt actcattata 3240
cgagttgggg ataccaacgg aacgagcata ctgtatcataa cttaaccagt ctcccgacag 3300
ttgcattcccc tttagat tcaacttgc tcacgaggaa gacgaagata gctgtctgaa 3360
agcaggagtt tacaatgtgg atggggatga aacagtaccg gtcctaaatgtc cccggatcat 3420
gtgtgcggaaa gctgtggcggtt gcaagacaag attcaaccct tccggaaatca agacttata 3480
aagagaatac aatcacttgc cgcggctaa cctgttggaa gggcgcggaa cgcagagttgg 3540
tgccccatgtt gatatcatgg gaaacttgc ttgtatgc gatatcatga ggggttgc 3600
cgaggttaac gggctgtata taggacatga ccaggtccac tctggcatat ttgaatggc 3660
ggagcgtatt gacctgaagc tgtga 3685

<210> 5
<211> 2427
<212> cDNA
<213> *Arabidopsis thaliana*

<400> 5

agaaaacagct ctttgtctct ctcgactgat ctaacaatcc ctaatctgtg ttctaaattc 60
 ctggacgaga tttgacaaag tccgtatagc ttaacctgggt ttaatttcaa gtgacagata 120
 tgccccttat tcatacgaaaa aagccgacgg agaaaccatc gacgcgcgc tctgaagagg 180
 tggtgacgca tgaggattcg caaaaagaaac cacacgaatc ttccaaatcc caccataaga 240
 aatcgaacgg aggagggaaag tggctgtca tcgattcttgc ttgttgggtt attgggtgtg 300
 tgtgtgtaac ctggtggtt cttcttcc tttacaacgc aatgcctgcg agctccctc 360
 agtatgtaac ggagcgaatc acgggtcctt tgcctgaccc gcccgggtt aagctaaaaa 420
 aaagaaggta ttaaggcgaa acatcctgtt gtcttcattc ctgggattgtt caccgggtgg 480
 ctcgagctt gggaaaggca acaatgcgtt gatggtttat ttagaaaacg tttgtgggt 540
 ggaacttttgc tgaagtcta caaaaaggctt ctatgttggg tggAACACAT gtcacttgac 600
 aatgaaactg gttggatcc agctggattt agagttcgag ctgtatcagg actcgtggct 660
 gctgactact ttgctcctgg ctactttgtc tggcagtgc tgattgtcaa cttgcacat 720
 attggatatg aagagaaaaa tatgtacatg gctgcataatg actggcggct ttcgtttcag 780
 aacacagagg tacgtgatca gactcttagc cgtagaaaaa gtaatataga gttgatggtt 840
 tctaccaacg gtggaaaaaa agcagttata gttccgcatt ccatgggggtt ctgtatTTT 900
 ctacattttt tgaagtgggt tgaggcacca gctcctctgg gtggcggggg tggccagat 960
 tggtgcaaa agtataattaa ggcggtgatg aacattgggtt gaccatttct tggtggttcca 1020
 aaagctgttgc cagggcttt ctctgctgaa gcaaggatg ttgcagttgc cagagcgatt 1080
 gccccaggat tcttagacac cgatataattt agacttcaga cttgcagca tggatgaga 1140
 atgacacgca catgggactc aacaatgtct atgttaccga agggaggtga cacgatatgg 1200
 ggcgggctt attggtcacc ggagaaaggc cacacctgtt gtggaaaaaa gcaaaagaac 1260
 aacgaaactt gtggtaagc aggtggaaaac ggagtttcca agaaaagtcc tggtaatcat 1320
 ggaaggatga tatctttgg gaaagaagta gcagaggctg cgcacatctga gattaataat 1380
 attgattttc gaggtgctgt caaaggctc agtataccaa atcacacctg tcgtgacgtg 1440
 tggacagagt accatgacat gggattgtt gggatcaaag ctatcgctga gtataaggc 1500
 tacactgctg gtggagctat agatctacta cattatgtt ctcctaagat gatggcgcgt 1560
 ggtggcgtc atttcttta tggaaattgtt gatgatttgg atgacaccaa gtatcaagat 1620
 cccaaataact ggtcaaatcc gtttagagaca aaattaccga atgctcctga gatggaaatc 1680
 tactcattat acggagtggg gataccaacg gaacgagcat acgtatacaa gcttaaccag 1740
 tctccgaca gttgcatccc cttttagata ttcaattctg ctcacgagga ggacgaagat 1800
 agctgtctga aagcaggagt ttacaatgtt gatggggatg aaacagtacc cgtcctaagt 1860
 gccgggtaca tggtgcaaa agcgtggcgt ggcaagacaa gattcaaccc ttccggaaatc 1920
 aagacttata taagagaata caatcactt cccggcgtt acctgttggg agggcgcggg 1980
 acgcagagtgt gtggccatgt tgatatcatg ggaaactttt ctttgatcga agatatcatg 2040
 aggggttgcg ccggaggtaa cgggtctgtt ataggacatg accaggtcca ctctggcata 2100
 tttgaatgggtt cggagcgtat tgacctgtt gatgttggat catgtatctt ttaagctgtc 2160
 ctgtcagctt atgtgaatcc aatacttttga aagagagatc atcatcaattt catcatcatc 2220
 gtcatcatca tgatgtctaa ctcacaaaga agcctgagaa tgatactttt gtcgaaattt 2280
 ctcaataacctt ctttaatattt cttattgtt gtaaattata caatcctatc taatgttga 2340
 acgataacac aaaacttgct gcnccatgt ttgtttgtt tggtaaaagc atcaatttgg 2400
 gggttaaaaaa aaaaaaaaaa aaaaaaaaaa 2427

<210> 6

<211> 671

<212> PRT

<213> Arabidopsis thaliana

<400> 6

Met	Pro	Leu	Ile	His	Arg	Lys	Lys	Pro	Thr	Glu	Lys	Pro	Ser	Thr	Pro
1								10					15		

Pro	Ser	Glu	Glu	Val	Val	His	Asp	Glu	Asp	Ser	Gln	Lys	Lys	Pro	His
20								25					30		

Glu Ser Ser Lys Ser His His Lys Lys Ser Asn Gly Gly Lys Trp

35	40	45
Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr		
50	55	60
Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro		
65	70	75
Gln Tyr Val Thr Glu Arg Ile Thr Gly Pro Leu Pro Asp Pro Pro Gly		
85	90	95
Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe		
100	105	110
Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln		
115	120	125
Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly		
130	135	140
Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp		
145	150	155
Asn Glu Thr Gly Leu Asp Pro Ala Gly Ile Arg Val Arg Ala Val Ser		
165	170	175
Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala		
180	185	190
Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met		
195	200	205
Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val		
210	215	220
Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val		
225	230	235
Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly		
245	250	255
Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro		
260	265	270
Leu Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala		
275	280	285
Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala		
290	295	300
Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile		
305	310	315
Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln		
325	330	335

His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu
 340 345 350

Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu
 355 360 365

Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys
 370 375 380

Gly Glu Ala Gly Glu Asn Gly Val Ser Lys Lys Ser Pro Val Asn Tyr
 385 390 395 400

Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser
 405 410 415

Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile
 420 425 430

Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly
 435 440 445

Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly
 450 455 460

Glu Ala Ile Asp Leu Leu His Tyr Val Ala Pro Lys Met Met Ala Arg
 465 470 475 480

Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr
 485 490 495

Lys Tyr Gln Asp Pro Lys Tyr Trp Ser Asn Pro Leu Glu Thr Lys Leu
 500 505 510

Pro Asn Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile
 515 520 525

Pro Thr Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser
 530 535 540

Cys Ile Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp
 545 550 555 560

Ser Cys Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val
 565 570 575

Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys
 580 585 590

Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn
 595 600 605

His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly
 610 615 620

Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met
 625 630 635 640

Arg Val Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val
645 650 655

His Ser Gly Ile Phe Glu Trp Ser Glu Arg Ile Asp Leu Lys Leu
660 665 670

<210> 7
 <211> 643
 <212> cDNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(402)

<400> 7

cg	gag	aaa	ata	gct	gct	ttg	aag	ggg	ggt	gtt	tac	tta	gcc	gat	ggt		48
Arg	Glu	Lys	Ile	Ala	Ala	Leu	Lys	Gly	Gly	Val	Tyr	Leu	Ala	Asp	Gly		
1				5						10				15			

gat gaa act gtt cca gtt ctt agt gcg ggc tac atg tgt gcg aaa gga 96
 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
 20 25 30

tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg 144
 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 35 40 45

aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc 192
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60

acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240
 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80

gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt 288
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
 85 90 95

ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa 336
 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
 100 105 110

ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att 384
 Leu Lys Leu
 115

gcg ttc caa agt gtc ctg cctgagtgca actctggatt ttgcttaat 432

attgttaattt ttcacgcttc attcgtccct ttgtcaaatt tacatttgac aggacgccaa 492

tgcgatacga tgttgtaccg ctatttcag cattgtatat taaactgtac aggtgtaaat 552

tgcatttgcc agctgaaatt gtgttagtcgt tttctttacg attaatanc aagtggcgaa 612

gcagtgcccc aagcnaaaaa aaaaaaaaaa a 643

<210> 8
<211> 115
<212> PRT
<213> Zea mays

<400> 8

Arg	Glu	Lys	Ile	Ala	Ala	Leu	Lys	Gly	Gly	Val	Tyr	Leu	Ala	Asp	Gly
1						5				10					15
Asp	Glu	Thr	Val	Pro	Val	Leu	Ser	Ala	Gly	Tyr	Met	Cys	Ala	Lys	Gly
						20				25					30
Trp	Arg	Gly	Lys	Thr	Arg	Phe	Ser	Pro	Ala	Gly	Ser	Lys	Thr	Tyr	Val
						35				40					45
Arg	Glu	Tyr	Ser	His	Ser	Pro	Pro	Ser	Thr	Leu	Leu	Glu	Gly	Arg	Gly
						50				55					60
Thr	Gln	Ser	Gly	Ala	His	Val	Asp	Ile	Met	Gly	Asn	Phe	Ala	Leu	Ile
						65				70					80
Glu	Asp	Val	Ile	Arg	Ile	Ala	Ala	Gly	Ala	Thr	Gly	Glu	Glu	Ile	Gly
						85				90					95
Gly	Asp	Gln	Val	Tyr	Ser	Asp	Ile	Phe	Lys	Trp	Ser	Glu	Lys	Ile	Lys
						100				105					110
Leu	Lys	Leu													
						115									

<210> 9
<211> 616
<212> cDNA
<213> Neurospora crassa

<400> 9

ggtggcgaag	acganggcgg	aagtggagg	ctaacgagaa	tgacnctcg	agatggatct	60
accctctaga	gacacgacta	ccnttgcacc	cagcctcaag	gtntacngtt	tntatggta	120
ggaagccgac	ggagcgagcc	tacatctatc	tggcgcccga	tcccgggacg	acaacgcac	180
tttagatgac	gatcgatacg	actttgactn	aggggcacat	tgaccacggt	gtgattttgg	240
gcgaaggcga	tggcacagt	aaccttatga	gtttgggta	cctgtgcaat	aaggggtgga	300
aaatgaagag	atacaatcct	gcgggctcaa	aaataaccgt	ggtcgagatg	ccgcatgaac	360
cagaacggtt	caatccgaga	ggagggccga	atacggcgg	tcacgtggat	attcttagaa	420
ggcagaatct	aaacgagttac	attcttaaag	tggcggcagg	tcgaggcgat	acaatttgggg	480
attttattac	tagtaatatt	cttaaatatg	tagaaaaggt	tgaatttat	gaagagtaat	540
taaatacggc	acataggtt	ctcaatagta	tgactaatta	aaaaaaaatt	ttttttctaa	600
aaaaaaaaaa	aaaaaaa					616

<210> 10
<211> 1562
<212> genomic DNA
<213> Arabidopsis thaliana

<400> 10

atgaaaaaaaaa	tatcttcaca	ttattcggta	gtcatagcga	tactcggtgt	ggtgacgatg	60
acctcgatgt	gtcaagctgt	gggttagcaac	gtgtaccctt	tgattctgg	tccagggaaac	120
ggaggttaacc	agcttagaggt	acggctggac	agagaataca	agccaagtag	tgtctgggt	180
agcagctgg	tatatccgt	tcataagaag	agtgggtggat	ggtttaggct	atggttcgat	240
gcagcagtgt	tattgtctcc	cttcaccagg	tgcttcagcg	atcgaatgtat	gttgtactat	300
gaccctgatt	tggatgatta	ccaaaatgt	cctgggtgtcc	aaacccgggt	tcctcatttc	360
ggttcggacca	aatcacttct	atacctcgac	cctcgtctcc	ggttagtact	ttccaagata	420
tatcattttg	ggacatttgc	ataatgaaca	aaatagacat	aaatttgggg	gattattgtt	480

atatcaatat ccatttatat gctagtcggt aatgtgagtg ttatgttagt atagttaatg 540
 tgagtgttat gtgattttcc attttaaatg aagctagaaa gttgtcggtt aataatgtt 600
 ctatgtcatg agaattataa ggacactatg taaatgttagc ttaataataa ggtttgattt 660
 gcagagatgc cacatcttac atggaacatt tggtaaaagc tctagagaaa aaatgcgggt 720
 atgttaacga ccaaaccatc ctaggagctc catatgattt caggtacggc ctggctgctt 780
 cgggccaccc gtcccgtgtc gcctcacagt tcctacaaga cctcaaacaa ttggtgaaa 840
 aaactagcag cgagaacgaa ggaaagccag tgatactcct ctccccatagc ctaggaggac 900
 tttcgtcct ccatttcctc aaccgtacca ccccttcatg gcgccgcaag tacatcaaac 960
 acttttgtc actcgctgctg ccattgggtg ggacgatctc tcagatgaag acatttgctt 1020
 ctggcaacac actcggtgtc ccttagtta accctttgtc ggtcagacgg catcagagga 1080
 cctccgagag taaccaatgg ctacttccat ctaccaaagt gtttcacgac agaactaaac 1140
 cgcttgcgt aactccccag gttaactaca cagcttacga gatggatcgg tttttgcag 1200
 acattggatt ctcacaagga gttgtgcctt acaagacaag agtgttgctt ttaacagagg 1260
 agctgatgac tccgggagtg ccagtcactt gcatatatgg gagaggagtt gatacaccgg 1320
 aggtttgtat gtatggaaaa ggaggattcg ataagcaacc agagattaag tatggagatg 1380
 gagatggac ggttaatttgcg cagcttgcgaa agtgcatacg ttgaacaccg 1440
 tagagattga tggagtttcg catacatcta tacttaaaga cgagatcgca cttaaagaga 1500
 ttatgaagca gatttcaatt attaattatg aattagccaa tgttaatgcc gtcaatgaat 1560
 ga 1562

<210> 11
 <211> 3896
 <212> genomic DNA
 <213> Arabidopsis thaliana

<400> 11
 atgggagcga attcgaaatc agtaacggct tccttcaccg tcacgcgtt tttttctt 60
 atttcggtg gccgaactgc ggtggaggat gagaccgagt ttcacggcga ctactcgaag 120
 ctatcgggtta taatcattcc gggatttgcg tcgacgcgc tacgagcgtg gtcgatcctt 180
 gactgtccat acactccgtt ggacttcaat ccgctcgacc tcgtatggct agacaccact 240
 aagggtccgtg atcttcattt ccttcgtcc ttattctgtc ggtcgagtca ctgttgatg 300
 aattccaagc gaaatatacg aatgaagcat gtctcgctc tcttattgtat tcgttcattt 360
 gtcaacagtg acgcttctga atctgagttt agagtcatat aaaacagctg actcggcgag 420
 tgtttccat cgcttttgtt tcgtaaatg tagcgcataat aatgtgtat tagtctgcgc 480
 tttttattca actagatctg caagtttcc agagtgcataat agttagtta gaaaatgtt 540
 ggtcatttttta cttgtgcatt gtgattctt tgggtgttgc ttactgatcg acgtgatgga 600
 tggtttacag cttctttctg ctgtcaactg ctggtttaag tggatgggtc tagatccta 660
 taatcaaaca gaccatccc agtgcataat acggcctgac agtgggtctt cagccatcac 720
 agaattggat ccaggttaca taacaggtat tttcgattt ttctttctt tgagtttct 780
 tcaatttgat atcatcttgc tggatataa tatggctaaat ttcatatattt tggtcaattt 840
 tcaggcctc tttctactgt ctggaaagag tggcttaatg ggtgtgttgc gtttggata 900
 gaagcaaatg caattgtcgc tgccatatac gattggagat tgcaccaac caaattggaa 960
 gagcgtgacc tttactttca caagctcaag ttagtcctt tcaggctaat gtcttttac 1020
 ttctttttt atgtaagata agctaagagc tctgggtcgtc ttcccttttgc caggttgacc 1080
 tttgaaactg cttaaaact ccgtggcgcc ccttctatag tatttgcctt ttcaatgggt 1140
 aataatgtct tcagatactt tctggatgg ctgaggctat aaattgcacc aaaacattat 1200
 ttgaagtggc ttgatcagca tatccatgtc tatttcgtt tgggtaccgg cctactatcc 1260
 ttaagttacc attttatattt ttctctatattt gggggagat tgggtgtact tactggattt 1320
 agctcgatac ctgatggat gttgatggat gagctcttct tctgggttgc gttgaggcaa 1380
 tcaaatactac tctctctgtt gtaacgtttt gccttcctgt ttctgagggtg acctctgact 1440
 tctcttttagt tttaagtagt tgatataac caggtcttataactcactgg attttcctt 1500
 tgaaagtatt actttgttta attgaactgc tgcgtacgcgtat atggtatctg tagatcttga 1560
 agtgcgtatgat atcaaagaac atattgtggg tagtataacct gtcagcggcc tttagctaaata 1620
 caacccaaacc acatgtacac tgatggat ttcagattat tattggtagac tttaagttga 1680
 gaagaaaactt tgactgaaat cttttattt taataggcta tgatgggtt attgaaatca 1740
 tgcgtacat tgcgtacat tttgttgc aaggcttcag ggaactgctc 1800

ggttgttgc caattcttt gcgtcgcat tgtggcttat gccatttca aagaattgca 1860
 agggtgataa cacattctgg acgcattttt ctgggggtgc tgcaaaagaaa gataagcgcg 1920
 tataccactg ttagtgaagag gaatatcaat caaaatattc tggctggccg acaaattatta 1980
 ttaacattga aattccttcc actagcggtt agactctgtat tatgcaactg taacactaac 2040
 aaaagttca ccaagaatgt tcactctcat attcgttcc tttgtatgtt atccatcagt 2100
 tacagaaaca gctctagtc acatgaccag catggaatgt ggccttccca ccctttgtc 2160
 tttcacagcc cgtgaactag cagatggac tctttcaaa gcaatagaag actatgaccc 2220
 agatagcaag aggatgttac accagttaaa gaagtagtgc ccttctttg tgataagaaa 2280
 tattgctcat cgatcatcac ttgctggc ttgtacgtc aaattgtttt gtttaaatct 2340
 ctatataat tggcatatgt ctgttctt cttactataa gaaacaagta taatcagaaa 2400
 ccttattatt gattatcgt tcttccttta tattatggaa tggcttttc gtttacagtt 2460
 atgaatgcaa aagggggtat tttagttgt tgattctctc attctctagt ttgttttgac 2520
 taatagcgtc aattttgtt ttcttagcaaa tctttgtgaa ttatataaa catgctaact 2580
 atactttca ggttgtatca tgatgaccct gtttttaatc ctctgactcc ttggagaga 2640
 ccacctataa aaaatgtatt ttgcataatat ggtgctcatc taaagacaga ggtatgatgc 2700
 attctcaata tcacattatg cgttgacttt gttattatat tccccatttg gtttgcataa 2760
 tcttttgaa ttatgattt tcttcctt tgcatctt gctattaagc gttaaaggt 2820
 ctaaatgtat gaagctgtct gtcataagggtt gtttattact ttgccccaaag tggcaaacct 2880
 tattctgata attggatcat cacggatatac atttatgaaa ctgaagggtt cctcggtca 2940
 aggttaatttt ccgcaatggc agaagtaaaa caggaaggca aagtcttctg tatcagtcta 3000
 gtggcatgtt atctcagtgt cataagcaaa ttattaaaca actaaaattt aagtactttt 3060
 ttatcattcc ttttgagctt agtggatgtt cagtggtttaa aagtggaaag aggtgttgca 3120
 tgaaacatga cacttgtatc aaagataact agcaaaacaa aactaaccctt tttctgaatt 3180
 tcatattatt aggagtagtc gtgttttaa aaaattttt ttaagaaacc gaaaaactag 3240
 ttcatatctt gattgtgcaat tatctgcagg tcttggactg tggttgtatgg gaacgctgga 3300
 cctataactg gggatgagac ggtaagctca gaagttgggtt ttgaaatttat ctcttgca 3360
 actactgaag actaagataa tacttgcttc tggAACACTG CTTGTATGT TCTCTAGTAC 3420
 actgcaatat tgactctccg ctacttttat tgattatgaa attgatctt tataaggtaacc 3480
 ctatcattca ctctcttggt gcaagaattt gctcgacactt aaagtttaca taacaatggc 3540
 tccccaggta ctcttttttta gttcctcacc ttatataat caaactttaa gtgtactttt 3600
 ctgggtatgt gttgatttac ctccaatttg ttctttctaa aaatcatata tctctgtact 3660
 cctcaagaac ttgtttaat ctaaacgaga ttctcattgg gaaaataaaaa caacagccag 3720
 aacacgatgg aagcgacgtt catgtggaaat taaatgttga tcatgagcat gggtcagaca 3780
 tcatagctaa catgacaaaaa gcaccaagggtt ttaagtacat aaccttttat gaagactctg 3840
 agagcattcc gggaaagaga acccgactt gggagcttga taaaagtggg tattaa 3896

<210> 12
 <211> 709
 <212> cDNA
 <213> Lycopersicon esculentum

<400> 12
 ctggggccaa aagtgaacat aacaaggaca ccacagtcg agcatgtatgt tcagatgtac 60
 aagtgcattt aaatatacgat catcaacatg gtgaagatattt cattccaaat atgacaaatgt 120
 tacctacaat gaagtacata accttattatg aggatttgcg aagttttca gggacaagaa 180
 cagcagtttggagcttggatgttgcgaaatc acagggacat tgcgtatctt ccagcttgc 240
 tgcggggacttggatgttgcgaaatc acagggacat tgcgtatctt ccagcttgc 300
 ttacaaaagg tgggtcttgcgaaatc acagggacat tgcgtatctt ccagcttgc 360
 acattgttgcgaaatc acagggacat tgcgtatctt ccagcttgc 420
 tgggatttgcgaaatc acagggacat tgcgtatctt ccagcttgc 480
 tcaaaatttttgcgaaatc acagggacat tgcgtatctt ccagcttgc 540
 caacgatgttgcgaaatc acagggacat tgcgtatctt ccagcttgc 600
 tctacatcttgcgaaatc acagggacat tgcgtatctt ccagcttgc 660
 aacaagtttgcgaaatc acagggacat tgcgtatctt ccagcttgc 709

<210> 13
 <211> 623

<212> PRT
 <213> Schizosaccharomyces pombe

<400> 13
 Met Ala Ser Ser Lys Lys Ser Lys Thr His Lys Lys Lys Lys Glu Val
 1 5 10 15
 Lys Ser Pro Ile Asp Leu Pro Asn Ser Lys Lys Pro Thr Arg Ala Leu
 20 25 30
 Ser Glu Gln Pro Ser Ala Ser Glu Thr Gln Ser Val Ser Asn Lys Ser
 35 40 45
 Arg Lys Ser Lys Phe Gly Lys Arg Leu Asn Phe Ile Leu Gly Ala Ile
 50 55 60
 Leu Gly Ile Cys Gly Ala Phe Phe Ala Val Gly Asp Asp Asn Ala
 65 70 75 80
 Val Phe Asp Pro Ala Thr Leu Asp Lys Phe Gly Asn Met Leu Gly Ser
 85 90 95
 Ser Asp Leu Phe Asp Asp Ile Lys Gly Tyr Leu Ser Tyr Asn Val Phe
 100 105 110
 Lys Asp Ala Pro Phe Thr Thr Asp Lys Pro Ser Gln Ser Pro Ser Gly
 115 120 125
 Asn Glu Val Gln Val Gly Leu Asp Met Tyr Asn Glu Gly Tyr Arg Ser
 130 135 140
 Asp His Pro Val Ile Met Val Pro Gly Val Ile Ser Ser Gly Leu Glu
 145 150 155 160
 Ser Trp Ser Phe Asn Asn Cys Ser Ile Pro Tyr Phe Arg Lys Arg Leu
 165 170 175
 Trp Gly Ser Trp Ser Met Leu Lys Ala Met Phe Leu Asp Lys Gln Cys
 180 185 190
 Trp Leu Glu His Leu Met Leu Asp Lys Lys Thr Gly Leu Asp Pro Lys
 195 200 205
 Gly Ile Lys Leu Arg Ala Ala Gln Gly Phe Glu Ala Ala Asp Phe Phe
 210 215 220
 Ile Thr Gly Tyr Trp Ile Trp Ser Lys Val Ile Glu Asn Leu Ala Ala
 225 230 235 240
 Ile Gly Tyr Glu Pro Asn Asn Met Leu Ser Ala Ser Tyr Asp Trp Arg
 245 250 255

Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu
 260 265 270
 Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val
 275 280 285
 Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys
 290 295 300
 Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Pro Thr Trp Val Asn
 305 310 315 320
 Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala
 325 330 335
 Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly
 340 345 350
 Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu
 355 360 365
 Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro
 370 375 380
 Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser
 385 390 395 400
 Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp
 405 410 415
 Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp
 420 425 430
 Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala
 435 440 445
 Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp
 450 455 460
 Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile
 465 470 475 480
 Tyr Cys Val His Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Tyr Tyr
 485 490 495
 Thr Asn Asn Pro Glu Gly Gln Pro Val Ile Asp Ser Ser Val Asn Asp
 500 505 510
 Gly Thr Lys Val Glu Asn Gly Ile Val Met Asp Asp Gly Asp Gly Thr
 515 520 525
 Leu Pro Ile Leu Ala Leu Gly Leu Val Cys Asn Lys Val Trp Gln Thr
 530 535 540
 Lys Arg Phe Asn Pro Ala Asn Thr Ser Ile Thr Asn Tyr Glu Ile Lys
 545 550 555 560

His Glu Pro Ala Ala Phe Asp Leu Arg Gly Gly Pro Arg Ser Ala Glu
 565 570 575

His Val Asp Ile Leu Gly His Ser Glu Leu Asn Glu Ile Ile Leu Lys
 580 585 590

Val Ser Ser Gly His Gly Asp Ser Val Pro Asn Arg Tyr Ile Ser Asp
 595 600 605

Ile Gln Glu Ile Ile Asn Glu Ile Asn Leu Asp Lys Pro Arg Asn
 610 615 620

<210> 14

<211> 432

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Lys Lys Ile Ser Ser His Tyr Ser Val Val Ile Ala Ile Leu Val
 1 5 10 15

Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr
 20 25 30

Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg
 35 40 45

Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu
 50 55 60

Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp
 65 70 75 80

Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met
 85 90 95

Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly
 100 105 110

Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr
 115 120 125

Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val
 130 135 140

Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu
 145 150 155 160

Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro
 165 170 175

Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu
 180 185 190

Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His
 195 200 205

Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro
 210 215 220
 Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro
 225 230 235 240
 Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr
 245 250 255
 Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg
 260 265 270
 Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His
 275 280 285
 Asp Arg Thr Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala
 290 295 300
 Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val
 305 310 315 320
 Val Pro Tyr Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr
 325 330 335
 Pro Gly Val Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro
 340 345 350
 Glu Val Leu Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile
 355 360 365
 Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala
 370 375 380
 Leu Lys Val Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His
 385 390 395 400
 Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln
 405 410 415
 Ile Ser Ile Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu
 420 425 430

 <210> 15
 <211> 552
 <212> PRT
 <213> Arabidopsis thaliana

 <400> 15
 Met Gly Ala Asn Ser Lys Ser Val Thr Ala Ser Phe Thr Val Ile Ala
 1 5 10 15
 Val Phe Phe Leu Ile Cys Gly Gly Arg Thr Ala Val Glu Asp Glu Thr
 20 25 30

Glu Phe His Gly Asp Tyr Ser Lys Leu Ser Gly Ile Ile Ile Pro Gly
 35 40 45

Phe Ala Ser Thr Gln Leu Arg Ala Trp Ser Ile Leu Asp Cys Pro Tyr
 50 55 60

Thr Pro Leu Asp Phe Asn Pro Leu Asp Leu Val Trp Leu Asp Thr Thr
 65 70 75 80

Lys Leu Leu Ser Ala Val Asn Cys Trp Phe Lys Cys Met Val Leu Asp
 85 90 95

Pro Tyr Asn Gln Thr Asp His Pro Glu Cys Lys Ser Arg Pro Asp Ser
 100 105 110

Gly Leu Ser Ala Ile Thr Glu Leu Asp Pro Gly Tyr Ile Thr Gly Pro
 115 120 125

Leu Ser Thr Val Trp Lys Glu Trp Leu Lys Trp Cys Val Glu Phe Gly
 130 135 140

Ile Glu Ala Asn Ala Ile Val Ala Val Pro Tyr Asp Trp Arg Leu Ser
 145 150 155 160

Pro Thr Lys Leu Glu Glu Arg Asp Leu Tyr Phe His Lys Leu Lys Leu
 165 170 175

Thr Phe Glu Thr Ala Leu Lys Leu Arg Gly Gly Pro Ser Ile Val Phe
 180 185 190

Ala His Ser Met Gly Asn Asn Val Phe Arg Tyr Phe Leu Glu Trp Leu
 195 200 205

Arg Leu Glu Ile Ala Pro Lys His Tyr Leu Lys Trp Leu Asp Gln His
 210 215 220

Ile His Ala Tyr Phe Ala Val Gly Ala Pro Leu Leu Gly Ser Val Glu
 225 230 235 240

Ala Ile Lys Ser Thr Leu Ser Gly Val Thr Phe Gly Leu Pro Val Ser
 245 250 255

Glu Gly Thr Ala Arg Leu Leu Ser Asn Ser Phe Ala Ser Ser Leu Trp
 260 265 270

Leu Met Pro Phe Ser Lys Asn Cys Lys Gly Asp Asn Thr Phe Trp Thr
 275 280 285

His Phe Ser Gly Gly Ala Ala Lys Lys Asp Lys Arg Val Tyr His Cys
 290 295 300

Asp Glu Glu Glu Tyr Gln Ser Lys Tyr Ser Gly Trp Pro Thr Asn Ile
 305 310 315 320

Ile Asn Ile Glu Ile Pro Ser Thr Ser Ala Arg Glu Leu Ala Asp Gly
 325 330 335

Thr Leu Phe Lys Ala Ile Glu Asp Tyr Asp Pro Asp Ser Lys Arg Met
 340 345 350

Leu His Gln Leu Lys Lys Tyr Val Pro Phe Phe Val Ile Arg Asn Ile
 355 360 365

Ala His Arg Ser Ser Leu Ala Gly Phe Leu Leu Tyr His Asp Asp Pro
 370 375 380

Val Phe Asn Pro Leu Thr Pro Trp Glu Arg Pro Pro Ile Lys Asn Val
 385 390 395 400

Phe Cys Ile Tyr Gly Ala His Leu Lys Thr Glu Val Gly Tyr Tyr Phe
 405 410 415

Ala Pro Ser Gly Lys Pro Tyr Pro Asp Asn Trp Ile Ile Thr Asp Ile
 420 425 430

Ile Tyr Glu Thr Glu Gly Ser Leu Val Ser Arg Ser Gly Thr Val Val
 435 440 445

Asp Gly Asn Ala Gly Pro Ile Thr Gly Asp Glu Thr Val Pro Tyr His
 450 455 460

Ser Leu Ser Trp Cys Lys Asn Trp Leu Gly Pro Lys Val Asn Ile Thr
 465 470 475 480

Met Ala Pro Gln Ile Leu Ile Gly Lys Ile Lys Gln Gln Pro Glu His
 485 490 495

Asp Gly Ser Asp Val His Val Glu Leu Asn Val Asp His Glu His Gly
 500 505 510

Ser Asp Ile Ile Ala Asn Met Thr Lys Ala Pro Arg Val Lys Tyr Ile
 515 520 525

Thr Phe Tyr Glu Asp Ser Glu Ser Ile Pro Gly Lys Arg Thr Ala Val
 530 535 540

Trp Glu Leu Asp Lys Ser Gly Tyr
 545 550

<210> 16

<211> 661

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80

Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95

Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110

Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125

Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140

Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160

Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175

Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190

Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205

Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220

Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240

Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255

Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270

Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285

Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300

Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320

Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335

Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365

Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430

Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445

Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480

Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495

Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525

Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540

Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560

Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605

Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

Met Pro Phe Pro Met
660

<210> 17

<211> 387

<212> PRT

<213> Arabidopsis thaliana

<400> 17

Val	Gly	Ser	Asn	Val	Tyr	Pro	Leu	Ile	Leu	Val	Pro	Gly	Asn	Gly	Gly
1				5						10			15		

Asn	Gln	Leu	Glu	Val	Arg	Leu	Asp	Arg	Glu	Tyr	Lys	Pro	Ser	Ser	Val
				20				25			30				

Trp	Cys	Ser	Ser	Trp	Leu	Tyr	Pro	Ile	His	Lys	Lys	Ser	Gly	Gly	Trp
				35			40			45					

Phe	Arg	Leu	Trp	Phe	Asp	Ala	Ala	Val	Leu	Leu	Ser	Pro	Phe	Thr	Arg
				50			55			60					

Cys	Phe	Ser	Asp	Arg	Met	Met	Leu	Tyr	Tyr	Asp	Pro	Asp	Leu	Asp	Asp
				65			70			75			80		

Tyr	Gln	Asn	Ala	Pro	Gly	Val	Gln	Thr	Arg	Val	Pro	His	Phe	Gly	Ser
				85				90			95				

Thr	Lys	Ser	Leu	Leu	Tyr	Leu	Asp	Pro	Arg	Leu	Arg	Asp	Ala	Thr	Ser
				100				105			110				

Tyr	Met	Glu	His	Leu	Val	Lys	Ala	Leu	Glu	Lys	Lys	Cys	Gly	Tyr	Val
				115				120			125				

Asn	Asp	Gln	Thr	Ile	Leu	Gly	Ala	Pro	Tyr	Asp	Phe	Arg	Tyr	Gly	Leu
				130			135			140					

Ala	Ala	Ser	Gly	His	Pro	Ser	Arg	Val	Ala	Ser	Gln	Phe	Leu	Gln	Asp
				145			150			155			160		

Leu	Lys	Gln	Leu	Val	Glu	Lys	Thr	Ser	Ser	Glu	Asn	Glu	Gly	Lys	Pro
				165				170			175				

Val	Ile	Leu	Leu	Ser	His	Ser	Leu	Gly	Gly	Leu	Phe	Val	Leu	His	Phe
				180				185			190				

Leu	Asn	Arg	Thr	Thr	Pro	Ser	Trp	Arg	Arg	Lys	Tyr	Ile	Lys	His	Phe
				195			200			205					

Val	Ala	Leu	Ala	Ala	Pro	Trp	Gly	Gly	Thr	Ile	Ser	Gln	Met	Lys	Thr
				210			215			220					

Phe	Ala	Ser	Gly	Asn	Thr	Leu	Gly	Val	Pro	Leu	Val	Asn	Pro	Leu	Leu
				225			230			235			240		

Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro
 245 250 255

 Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu Val Val Thr Pro
 260 265 270

 Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile
 275 280 285

 Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg Val Leu Pro Leu
 290 295 300

 Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr Cys Ile Tyr Gly
 305 310 320

 Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly Lys Gly Phe
 325 330 335

 Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn
 340 345 350

 Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu Asn Thr Val Glu
 355 360 365

 Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu
 370 375 380

 Lys Glu Ile
 385

<210> 18
<211> 389
<212> PRT
<213> Arabidopsis thaliana

<400> 18
Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe Ile Pro
 1 5 10 15

Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln Cys Ala
 20 25 30

Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Leu Cys Trp
 35 40 45

Val Glu His Met Ser Leu Asp Asn Glu Thr Gly Leu Asp Pro Ala Gly
 50 55 60

Ile Arg Val Arg Ala Val Ser Gly Leu Val Ala Ala Asp Tyr Phe Ala
 65 70 75 80

Pro Gly Tyr Phe Val Trp Ala Val Leu Ile Ala Asn Leu Ala His Ile
 85 90 95

Gly Tyr Glu Glu Lys Asn Met Tyr Met Ala Ala Tyr Asp Trp Arg Leu
 100 105 110

Ser Phe Gln Asn Thr Glu Arg Asp Gln Thr Leu Ser Arg Met Lys Ser
 115 120 125
 Asn Ile Glu Leu Met Val Ser Thr Asn Gly Gly Lys Lys Ala Val Ile
 130 135 140
 Val Pro His Ser Met Gly Val Leu Tyr Phe Leu His Phe Met Lys Trp
 145 150 155 160
 Val Glu Ala Pro Ala Pro Leu Gly Gly Gly Pro Asp Trp Cys
 165 170 175
 Ala Lys Tyr Ile Lys Ala Val Met Asn Ile Gly Gly Pro Phe Leu Gly
 180 185 190
 Val Pro Lys Ala Val Ala Gly Leu Phe Ser Ala Glu Ala Lys Asp Met
 195 200 205
 Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu Pro Lys Gly
 210 215 220
 Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu Leu Pro Asn
 225 230 235 240
 Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile Pro Thr
 245 250 255
 Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser Cys Ile
 260 265 270
 Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp Ser Cys
 275 280 285
 Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val Pro Val
 290 295 300
 Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys Thr Arg
 305 310 315 320
 Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn His Ser
 325 330 335
 Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly Ala His
 340 345 350
 Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met Arg Val
 355 360 365
 Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val His Ser
 370 375 380
 Gly Ile Phe Glu Trp
 385

<210> 19
 <211> 1986
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1983)

<400> 19

atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct	48
Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser	
1 5 10 15	
gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga	96
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg	
20 25 30	
aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt	144
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly	
35 40 45	
att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg	192
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg	
50 55 60	
aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg	240
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu	
65 70 75 80	
att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt	288
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe	
85 90 95	
ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt	336
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe	
100 105 110	
gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt	384
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val	
115 120 125	
ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac	432
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn	
130 135 140	
tac tcc aca tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt	480
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly	
145 150 155 160	
aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta	528
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val	
165 170 175	
atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att	576
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile	

180

185

190

gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp 195	200	205	624
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp 210	215	220	672
ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn 225	230	235	720
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile 245	250	255	768
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile 260	265	270	816
ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu 275	280	285	864
gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys 290	295	300	912
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu 305	310	315	960
att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp 325	330	335	1008
gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val 340	345	350	1056
aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly 355	360	365	1104
gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr 370	375	380	1152
att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser 385	390	395	1200

aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser 405 410 415	1248
atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct Met Leu Pro Lys Gly Glu Val Ile Trp Gly Asp Met Lys Ser Ser 420 425 430	1296
tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att Ser Glu Asp Ala Leu Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile 435 440 445	1344
cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met 450 455 460	1392
aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln 465 470 475 480	1440
aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu 485 490 495	1488
gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met 500 505 510	1536
gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr 515 520 525	1584
ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp 530 535 540	1632
gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro 545 550 555 560	1680
gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser 565 570 575	1728
atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly 580 585 590	1776
att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp 595 600 605	1824
ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser 610 615 620	1872

gct gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp 625 630 635 640	1920
ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln 645 650 655	1968
atg ccc ttc cca atg taa Met Pro Phe Pro Met 660	1986
<210> 20	
<211> 661	
<212> PRT	
<213> <i>Saccharomyces cerevisiae</i>	
<400> 20	
Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser 1 5 10 15	
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg 20 25 30	
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly 35 40 45	
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg 50 55 60	
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu 65 70 75 80	
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe 85 90 95	
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe 100 105 110	
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val 115 120 125	
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn 130 135 140	
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly 145 150 155 160	
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val 165 170 175	
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile 180 185 190	
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp 195 200 205	

Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Arg Gly Trp Val
 340 345 350
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655
 Met Pro Phe Pro Met
 660

<210> 21
 <211> 1986
 <212> DNA
 <213> *Saccharomyces cerevisiae*
 <220>
 <221> CDS
 <222> (1)..(1983)
 <400> 21
 atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15
 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30
 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45
 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu 65 70 75 80	240
att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe 85 90 95	288
ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe 100 105 110	336
gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val 115 120 125	384
ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn 130 135 140	432
tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly 145 150 155 160	480
aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val 165 170 175	528
atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile 180 185 190	576
gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp 195 200 205	624
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp 210 215 220	672
ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn 225 230 235 240	720
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile 245 250 255	768
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile 260 265 270	816
ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu 275 280 285	864

gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys 290 295 300	912
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu 305 310 315 320	960
att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp 325 330 335	1008
gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Arg Gly Trp Val 340 345 350	1056
aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly 355 360 365	1104
gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr 370 375 380	1152
att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser 385 390 395 400	1200
aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser 405 410 415	1248
atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct Met Leu Pro Lys Gly Glu Val Ile Trp Gly Asp Met Lys Ser Ser 420 425 430	1296
tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile 435 440 445	1344
cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met 450 455 460	1392
aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln 465 470 475 480	1440
aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu 485 490 495	1488
gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met 500 505 510	1536

gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr 515 520 525	1584
ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp 530 535 540	1632
gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro 545 550 555 560	1680
gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser 565 570 575	1728
atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly 580 585 590	1776
att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp 595 600 605	1824
ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser 610 615 620	1872
gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp 625 630 635 640	1920
ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln 645 650 655	1968
atg ccc ttc cca atg taa Met Pro Phe Pro Met 660	1986

<210> 22
<211> 661
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 22 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser 1 5 10 15
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg 20 25 30
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly 35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365

 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380

 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400

 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415

 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430

 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445

 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460

 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480

 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495

 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510

 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525

 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540

 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560

 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590

 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605

 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620

 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640

 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

Met Pro Phe Pro Met
660

<210> 23
<211> 2312
<212> genomic DNA
<213> *Schizosaccharomyces pombe*

<400> 23
atggcgtctt ccaagaagag caaaaactcat aaaaaaaaaga aagaagtcaa atccctatc 60
gacttaccaa attcaaagaa accaactcgc gcttgagtg agcaaccttc a诶ggtccgaa 120
acacaatctg tttcaaataa atcaagaaaa totaaatttg gaaaagatt gaattttata 180
ttggcgcta ttttggaat atgcggtgct tttttttcg ctgtggaga cgacaatgct 240
gttttcgacc ctgctacggt agataaattt gggatatgc taggctctc agacttgtt 300
gatgacatta aaggatattt atcttataat gtgttaagg atgcacccct tactacggac 360
aaggcttcgc agtctccatcg cgaaaaatgaa gtcagaattt gtcttgatat gtacaatgag 420
ggatatcgaa gtgaccatcc tggttattatg gttcctgggt ttatcagctc aggattagaa 480
agttggctgt ttaataattt ctcgattcct tacttagga aacgtctttg gggtagctgg 540
tctatgctga aggcaatggtt ctttgacaaag caatgctggc ttgaacattt aatgcttgat 600
aaaaaaaaaccg gcttggatcc gaagggatt aagctgcgag cagctcaggg gtttgaagca 660
gctgattttt ttatcacggg ctattggatt tggagtaaaag taattgaaaaa ctttgctgca 720
attggttatg agcctaataa catgttaagt gcttcttagt atggcggtt atcatatgca 780
aatttagagg aacgtgataa atattttca aagttaaaaa tgttcattga gtacagcaac 840
attgtacata agaaaaagggt agtgttgatt ttcactcca tgggttcaca gtttacgtac 900
tatTTTTTta agtgggttga agctgagggc tacggaaatg gtggaccgac ttgggttaat 960
gatcatattt aagcattttt aaatgtgagt ctcgatgggt gtttactac gtttctaact 1020
tttgaataga tatcgggatc tttgatttga gcacccaaaa cagtggcagc gttttatcg 1080
ggtgaardtga aagatacagg tattgttaatt acattaaaca tgttaatatt taattttgc 1140
taaccgtttt aagctcaattt gaatcagtt tcggctctatg ggtaagcaat aaattgttga 1200
gatttggcac taattttactg ttttagttgg aaaaattttt ttcccgttct gaggtatatt 1260
caaaaataca aatgtgctct acttttcttca acttttaataa gagagccatg atgggtcgca 1320
ctatgggagg agtagttct atgcttccat aaggaggcga tggttatgg gaaaatgc 1380
gttgggttaag aaatatgtgc tgttaatttt ttattaaatat ttaggctcca gatgatctt 1440
atcaaacaaa ttttccat ggtgcaattt ttcgatataag agaagacatt gataaggacc 1500
acgatgaatt tgacatagat gatgcattac aattttttaaa aaatgttaca gatgacgatt 1560
ttaaagtcat gctagcgaaa aattttccct acggcttgc ttggactgaa aaaaagtg 1620
taaaaaataa cgaaatgccg tctaaatggta taaatccgtt agaagtaaga acattaaagt 1680
tactaaattt tactaacccaa aatagacttag tcttccttat gctccgtata tgaaaaatttt 1740
ttgcgttcac ggggtcgaa aaccaactga gagaggttat tattatacta ataatcctga 1800
ggggcaacct gtcattgatt ctcggttaa tgatggaaaca aaagttgaaa atgtgagaga 1860
atttatgttt caaacattct attaactgtt ttatttaggtt attgttatgg atgatgggt 1920
tggaaacttta ccaatatttgc cccttgggtt ggtgtcaat aaagttggc aaacaaaaag 1980
gtttaatcct gctaatacaca gtatcacaaa ttatgaaatc aagcatgaac ctgctgcgtt 2040
tgatctgaga ggaggacctc gctcgccaga acacgtcgat atacttggac attcagagct 2100
aaatgtatgt tcattttacc ttacaaattt ctattactaa ctcttggaaat aaggaaat 2160
ttttaaaatgtt ttcattcaggc catggtgact cggtagccaa ccgttatata tcagatattc 2220
agtacggaca taagtttgtt agattgcaat taactaacta accgaacagg gaaataat 2280
atgagataaa tctcgataaa ccttagaaattt aa 2312

```
<210> 24
<211> 3685
<212> genomicDNA
<213> Arabidopsis thaliana
```

<400> 24

gtgtgcaaaa gcgtggcggt gcaagacaag attcaaccct tccggaatca agacttatat 3480
 aagagaatac aatcaactctc cgccggctaa cctgttgaa gggcgcgaaa cgtagtgg 3540
 tgcccattgtt gatatcatgg gaaactttgc tttgatcgaa gatatcatga gggttgccgc 3600
 cggaggtaac gggctgata taggacatga ccaggtccac tctggcatat ttgaatggtc 3660
 ggagcgtatt gacctaagc tgtga 3685

<210> 25

<211> 402

<212> cDNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (120)..(401)

<400> 25

agaaaacagct ctttgtctct ctcgactgat ctaacaatcc ctaatctgtg ttctaaattc 60

ctggacgaga tttgacaaag tccgtatagc ttaacctgggt ttaatttcaa gtgacagat 119

atg	ccc	ctt	att	cat	cg	aaa	aag	ccg	ac	g	aa	cc	tc	ac	cc		167
Met	Pro	Leu	Ile	His	Arg	Lys	Lys	Pro	Thr	Glu	Lys	Pro	Ser	Thr	Pro		
1	5							10					15				

cca	tct	gaa	gag	gt	gt	cac	gat	gag	gat	tc	caa	aag	aa	cc	cac		215
Pro	Ser	Glu	Glu	Val	Val	His	Asp	Glu	Asp	Ser	Gln	Lys	Lys	Pro	His		
20								25					30				

gaa	tct	tcc	aaa	tcc	cac	cat	aag	naa	tc	aa	g	g	g	gg	aag	tgg	263
Glu	Ser	Ser	Lys	Ser	His	His	Lys	Xaa	Ser	Asn	Gly	Gly	Gly	Lys	Trp		
35								40					45				

tcg	tgc	atc	gat	tct	tgt	tgt	tgg	ttc	att	ggg	tgt	gt	tgt	gt	acc		311
Ser	Cys	Ile	Asp	Ser	Cys	Cys	Trp	Phe	Ile	Gly	Cys	Val	Cys	Val	Thr		
50								55					60				

tgg	tgg	ttt	ctt	ctc	ttc	ttt	tac	aac	gca	atg	cct	g	agc	ttc	cct		359
Trp	Trp	Phe	Leu	Leu	Phe	Leu	Tyr	Asn	Ala	Met	Pro	Ala	Ser	Phe	Pro		
65								70			75		80				

cag	tat	gta	ac	g	gg	cc	aat	ca	g	ng	tcc	ttt	gcc	tta	ccc	g	402
Gln	Tyr	Val	Thr	Glu	Pro	Asn	His	Xaa	Ser	Phe	Ala	Leu	Pro				
85									90								

<210> 26

<211> 643

<212> cDNA

<213> Zea mays

<220>

<221> CDS

<222> (1)..(402)

<400> 26

cg_g gag aaa ata gct gct ttg aag ggg ggt gtt tac tta gcc gat ggt 48
 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
 1 5 10 15

gat gaa act gtt cca gtt ctt agt gcg ggc tac atg tgt gcg aaa gga 96
 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
 20 25 30

tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg 144
 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 35 40 45

aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc 192
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60

acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240
 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80

gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt 288
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
 85 90 95

ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa 336
 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
 100 105 110

ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att 384
 Leu Lys Leu
 115

gcg ttc caa agt gtc ctg cctgagtgca actctggatt ttgcttaat 432

attgttaattt ttcacgcttc attcgtccct ttgtcaaatt tacatttgac aggacgccaa 492

tgcgatacga tgttgtaccg ctatttcag cattgtatat taaaactgtac aggtgtaaatg 552

tgcatttgcc agctgaaatt gtgtagtcgt tttctttacg attaaatanc aagtggcgga 612

gcagtgc(cccccc aagcnaaaaa aaaaaaaaaa a 643

<210> 27
 <211> 115
 <212> PRT
 <213> Zea mays

<400> 30
 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
 1 5 10 15

Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
 20 25 30

Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 35 40 45

Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60

Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
 85 90 95
 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
 100 105 110
 Leu Lys Leu
 115

<210> 28
 <211> 516
 <212> cDNA
 <213> Neurospora crassa

<400> 28
 ggtggcgaag acganggcgg aagttggagg ctaacgagaa tgacnctcg 60
 accctctaga gacacgacta ccnttgcacc cagcctcaag gtn tacngtt tntatggta 120
 ggaagccgac ggagcggagcc tacatctatc tggcgcccga tcccgggacg acaacgcac 180
 ttttagatgac gatcgatacg actttgactn agggggcacat tgaccacgg 240
 gcgaaggcga tggcacagt 300
 gcaaggcga tggcacagt 300
 aaccttatga gtttgggta cctgtgcaat aagggggtgga 360
 aaatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcata 360
 cagaacggtt caatccgaga ggagggccga atacggcgg 420
 tgaaaattat gaagagtaat taaatacggc acataggta ctcaatagta tgactaatta 480
 aaaaaaaaaatt tttttctaa aaaaaaaaaa aaaaaaa 516

<210> 29
 <211> 1562
 <212> genomic DNA
 <213> Arabidopsis thaliana

<400> 29
 atgaaaaaaaa tatcttcaca ttattcggta gtcatagcga tactcggtt ggtgacgat 60
 acctcgatgt gtcaagctgt gggtagcaac gtgtaccctt tgattctgg 120
 ggaggtaacc agctagaggt acggctggac agagaataca agccaagtag tgtctgg 180
 agcagctgg 240
 tataatccat tcataagaag agtgggtggat ggtttaggct atggttcgat 240
 gcagcgtt tattgtctcc cttcaccagg tgcttcagcg atcgaatgat gttgtactat 300
 gaccctgatt tggatgatta ccaaatgtt cctgggtgtcc aaacccgggt tcctcatttc 360
 ggttcgacca aatcacttct atacctcgac cctcgtctcc ggttagtact ttccaagata 420
 tatacattttgc ataatgaaca aaatagacat aaatttggg gattattgtt 480
 atatacaatccat ccatttatat gctagtcgtt aatgtgagtg ttatgttagt atatgtat 540
 tgagtgttat gtgatttcc attttaatg aagctagaaa gttgtcg 600
 ctatgtcatg agaattataa ggacactatg taaatgttagc ttaataataa ggtttgattt 660
 gcagagatgc cacatcttac atgaaacatt tggtaaaagc tctagagaaa aaatgcggg 720
 atgttaacga ccaaaccatc ctaggagctc catatgattt caggtacggc ctggctgctt 780
 cggccaccc gtcgggtgt 840
 gtcgtgtgc gcctcacagt tcctacaaga cctcaaaca 840
 aaactagcag cgagaacgaa ggaaagccag tgatactcct ctccccatgc ctaggaggac 900
 ttttcgtctt ccatttcctc aaccgtacca ccccttcatg gcccggcaag tacatcaa 960
 actttgtgc actcgctgcg ccattgggtg ggacgatctc tcagatgaag acatggctt 1020
 ctggcaacac actcggtgtc ccttagtta accctttgct ggtcagacgg catcagagga 1080
 cctccgagag taaccaatgg ctacttccat ctaccaaaatg gtttcacgac agaactaaac 1140
 cgcttgcgt aactcccgag gtttaactaca cagttacga gatggatcg 1200
 acattggatt ctcacaagga gttgtgcctt acaagacaag agtgttgctt ttaacagagg 1260
 agctgatgac tccgggagtg ccagtca 1320
 gatgatgat gtatggaaaa ggaggattcg ataagcaacc agagattaag tatggagatg 1380
 gagatggac gtttaatttgc gtcgttgc 1440

tagagattga tggagtttcg catacatcta tacttaaaga cgagatcgca cttaaagaga 1500
 ttatgaagca gatttcaatt attaatttatg aattagccaa tgttaatgcc gtcaatgaat 1560
 ga 1562

<210> 30

<211> 3896

<212> genomic DNA

<213> Arabidopsis thaliana

<400> 30

atgggagcga attcgaatc agtaacggct tccttcaccg tcatacgccgt tttttcttg 60
 atttgcggtg gccgaactgc ggtggaggat gagaccgagt ttacacggcga ctactcgaaag 120
 ctatcggtta taatcattcc gggatttgcg tcgacgcagc tacgagcgtg gtcgatcctt 180
 gactgtccat acactccggt ggacttcaat ccgctcgacc tcgtatggct agacaccact 240
 aagggtccgtg atcttcattt ccttcgtcc ttattctgtc ggtcgagtca cttgttgcgt 300
 aattccaagc gaaatatagc aatgaagcat gtctcgctc tcttattgtat tcgttcatta 360
 gtcaacagtg acgcttctga atctgagttt agagtcatat aaaacagctg actcggcgag 420
 tgtttccat cgcttttgt tcgctaaatg tagcgcataatg aatgtgtaat tagtctgcgc 480
 tttttattca actagatctg caagttttc agagtgcataatgtagtta gaaaatgtta 540
 ggtcatttta cttgtgcatt gtgattctt tgggtgtgc ttactgatcg acgtgatgga 600
 tggtttacag cttcttctg ctgtcaactg ctgggttaag tggatgtgc tagatcctt 660
 taatcaaaca gaccatcccc agtgtaagtc acggcctgac agtggctttt cagccatcac 720
 agaattggat ccaggttaca taacaggtat ttcggattt ttctttctt tgagtttct 780
 tcaatttgcattt atcatcttgc atgtatataa tatggctaaat ttcattaaatt tggcaattt 840
 tcaggtccctc tttctactgt ctggaaagag tggcttaagt ggtgtgtga gtttggata 900
 gaagcaaatg caattgtcgc tggtccatac gattggagat tgcaccaac caaattggaa 960
 gagcgtgacc tttactttca caagctcaag ttagtccta tcaggctaat gtcttttatac 1020
 ttctctttt atgtaagata agctaagagc tctggtcgtc ttctttttt caggttgacc 1080
 tttgaaactg cttaaaact ccgtggcgcc ccttctatag tatttgccta ttcaatgggt 1140
 aataatgtct tcagatactt tctggatgg ctgaggctag aaattgcacc aaaacattat 1200
 ttgaagtggc ttgatcagca tatccatgtc tatttcgtg ttggtaaccgg cctactatcc 1260
 ttaagttacc attttattt ttctctaatt gggggagttt tggatgtact tactggattt 1320
 agctcgatac ctgattttgtt gttgatttag gagctccctc tctgggtct gttgaggca 1380
 tcaaataatctac tctctctggc gtaacgttt gccttcctgt ttctgaggtt acctctgact 1440
 tctctttatgt ttaagttgtt tgatataac caggctttat aactcactgg attttcctt 1500
 tgaaagtatt acttttgcattt attgaactgc tgcgtcgat atggatctg tagatcttgc 1560
 agtgcgtt atcaaagaac atattgtgg tagtataacct gtcagcggcc ttagctaata 1620
 caaccaaacc acatgtacac tgatttagtt ttcaagattat tggatgtac ttaagttga 1680
 gaagaaaactt tgactgaaat cttttattt taataggcta tgatttgcattt attgaaatca 1740
 tggacatcat tgacatgcgc ttctcatgtt tttgttggc aaggcttcag ggaactgctc 1800
 ggttgggtgc caattctttt ggcgtcgtcat tggcttat gccattttca aagaattgca 1860
 aggggtataa cacattctgg acgcattttt ctgggggtgc tgcaaaagaaa gataagcg 1920
 tataccactg tggatgaaagag gaatataat caaaatattt tggctggccg acaaataat 1980
 ttaacattga aattccttcc actagcggtt agactctgtat tggatgtact taacactaac 2040
 aaaagttca ccaagaatgt tcactctcat atttcgttcc tttgtatgtt atccatcagt 2100
 tacagaaaca gctctagtc acatgaccag catggatgt ggccttccca ccctttgtc 2160
 tttcacagcc cgtgaacttag cagatgggc tctttcaaa gcaatagaag actatgaccc 2220
 agatagcaag aggatgttac accagttaa gaagtgatgtt cttttcttgc tgataagaaa 2280
 tattgctcat cgtatcatc ac ttgtggctt cttgtacgtc aaattgtttt gtttaatct 2340
 ctatataat tggatgtatgc ctggatgtt cttactataa gaaacaagta taatcagaaa 2400
 ctttatttattt gattatcgt tcttcctta tattatggaa tggatgttgc ttacatgtt 2460
 atgaatgcaaa aagggggtat tttagttgtat tggatgttgc attctctgtt ttgttttgc 2520
 taatagcgatc aattttgttt ttcttagcaaa tctttgtgaa ttatataataa catgctaact 2580
 atactttca ggttgtatca tgatgaccct gtttttaatc ctctgactcc ttggggagaga 2640
 ccacctataa aaaatgttattt ttgcataat ggtgctcatac taaagacaga ggtatgtgc 2700
 attctcaata tcacattatg cggtactttt gttattatat tccccatttg gtttgcataa 2760

tctttttgaa	ttatgattta	tcttctccct	tgcatcttat	gctattaagc	gttaaaggta	2820
ctaatgtat	gaagctgtct	gtcatagggtt	ggttattact	ttggcccaag	tggcaaacct	2880
tatcctgata	attggatcat	cacggatatac	atttatgaaa	ctgaaggttc	cctcggtc	2940
aggttaattt	ccgcaatggc	agaagtaaaa	caggaaggca	aagtcttctg	tatcagtcta	3000
gtggcagttt	attcagttt	cataagcaaa	ttattaaaca	actaaaaattt	aagtactttt	3060
ttatcatcc	tttgagctt	agtggatgtat	cagtggctta	aagtggaaag	aggtgttgc	3120
tgaaacatga	cacttgtatc	aaagataact	agcaaaaacaa	aactaacc	tttctgaatt	3180
tcatattatt	aggagtagtc	gtgctttaa	aaaatttgtt	ttaagaaacc	aaaaaactag	3240
ttcataatctt	gattgtgcaa	tatctgcagg	tctggaaactg	tgggtatgg	gaacgctgga	3300
cctataactg	gggatgagac	ggtaagctca	gaagttggtt	ttgaaattat	cttcttgcaa	3360
actactgaag	actaaagataa	tacttgcttc	tggaacactg	cttgctatgt	tctctagtagc	3420
actgcaatat	tgactctccg	ctactttat	tgattatgaa	attgatctct	tataggtacc	3480
ctatcattca	ctctcttggt	gcaagaattt	gctcggacct	aaagttaaaca	taacaatg	3540
tccccaggtt	ctctttttta	gttcctcacc	ttatataat	caaactttaa	gtgtactttt	3600
ctggttatgt	gttgattttac	ctccaatttg	ttctttctaa	aaatcatata	tctctgtact	3660
cctcaagaac	ttgttataat	ctaaacgaga	ttctcattgg	aaaaataaaa	caacagccag	3720
aacacgatgg	aagcgacgtt	catgtgaac	taaatgttga	tcatgagcat	gggtcagaca	3780
tcatagctaa	catgacaaaa	gcaccaaggg	ttaagtacat	aacctttat	gaagactctg	3840
agacattcc	ggggaaagaga	accgcagtct	gggagcttga	taaaagtggg	tattaa	3896

<210> 31
<211> 709
<212> cDNA
<213> tomato

<210> 32
<211> 7
<212> PRT
<213> Conserved Sequence

<400> 7
Phe Xaa Lys Trp Val Glu Ala
1 5